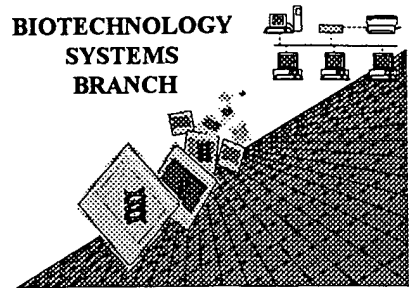


Hammond

RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/16775A
Art Unit / Team No. : 1646
Date Processed by STIC: 11/26/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/167,205

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 _____ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 _____ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 _____ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 _____ Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 _____ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 _____ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 _____ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.
- 8 _____ Skipped Sequences Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 _____ Skipped Sequences Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 _____ Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 _____ Use of <213>Organism Sequence(s) _____ are missing this mandatory field or its response.
(NEW RULES)
- 12 _____ Use of <220>Feature Sequence(s) _____ are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
 Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 _____ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

Hamuel

1646

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/167,705ADATE: 11/26/1999
TIME: 16:17:47

Input Set: I167705A.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

Does Not Comply
Corrected Diskette Needed

1 <110> APPLICANT: Schmidt, Ann Marie
2 Stern, David
3 <120> TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND
4 USES THEREOF
5 <130> FILE REFERENCE: 0575-55873
6 <140> CURRENT APPLICATION NUMBER: US/09/167,705A
7 <141> CURRENT FILING DATE: 1998-10-06
8 <160> NUMBER OF SEQ ID NOS: 6
9 <170> SOFTWARE: PatentIn Ver. 2.0
10 <210> SEQ ID NO 1
11 <211> LENGTH: 395
12 <212> TYPE: DNA
13 <213> ORGANISM: BOVINE
14 <400> SEQUENCE: 1
15 atgactaagc tggaggacca cctggaggga atcatcaaca tcttccacca gtactccgtt 60
16 cgggtggggc atttcgacac cctcaacaag cgtgagctga agcagctgat cacaaagga 120
17 acttcccaaa accctccaga acaccaaaga ccaacctacc attgacaaaa tattccaaga 180
18 cctggatgcc gataaagacg gagccgtcag ctttgaggaa ttcgtagtcc tgggtgccag 240
19 ggtgctgaaa acagcccaca tagatatcca caaagagtag gtttccagca atgttcccaa 300
20 gaagacttac ctttctctc cctgaggctg ctccccgagg gagagagaat tataaacgta 360
21 ctttggcaaa ttcttagcaa aaaaaaaaaa aaaaa 395
22 <210> SEQ ID NO 2
23 <211> LENGTH: 50
24 <212> TYPE: PRT
25 <213> ORGANISM: ARTIFICIAL SEQUENCE
26 <220> FEATURE:
27 <221> NAME/KEY: UNSURE
28 <222> LOCATION: (31) ? Xaa is at location 47
29 <223> OTHER INFORMATION: Xaa in this position is undetermined.
30 <400> SEQUENCE: 2
31 Thr Lys Leu Glu Asp His Leu Glu Gly Ile Ile Asn Ile Gly His Gln
32 1 5 10 15
33 Tyr Ser Val Arg Val Gly His Phe Asp Thr Leu Asn Lys Tyr Glu Leu
34 20 25 30
35 W--> Lys Gln Leu Gly Thr Lys Glu Leu Pro Lys Thr Leu Gln Asn Xaa Lys
36 35 40 45
37 Asp Gln
38 50
39 <210> SEQ ID NO 3
40 <211> LENGTH: 90
41 <212> TYPE: PRT
42 <213> ORGANISM: ARTIFICIAL SEQUENCE
43 <400> SEQUENCE: 3
44 Thr Lys Leu Glu Asp His Leu Glu Gly Ile Ile Asn Ile Phe His Gln

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/167,705ADATE: 11/26/1999
TIME: 16:17:47

Input Set: I167705A.RAW

45 1 5 10 15
46 Tyr Ser Val Arg Val Gly His Phe Asp Thr Leu Asn Lys Arg Glu Leu
47 20 25 30
48 Lys Gln Leu Ile Thr Lys Glu Leu Pro Lys Thr Leu Gln Asn Thr Lys
49 35 40 45
50 Asp Gln Pro Thr Ile Asp Lys Ile Phe Gln Asp Leu Asp Ala Asp Lys
51 50 55 60
52 Asp Gly Ala Val Ser Phe Glu Glu Phe Val Val Leu Val Ser Arg Val
53 65 70 75 80
54 Leu Lys Thr Ala His Ile Asp Ile His Lys
55 85 90

56 <210> SEQ ID NO 4

57 <211> LENGTH: 90

58 <212> TYPE: PRT

59 <213> ORGANISM: ARTIFICIAL SEQUENCE

60 <400> SEQUENCE: 4

61 Thr Lys Leu Glu Asp His Leu Glu Gly Ile Ile Asn Ile Phe His Gln
62 1 5 10 15
63 Tyr Ser Val Arg Val Gly His Phe Asp Thr Leu Asn Lys Arg Glu Leu
64 20 25 30
65 Lys Gln Leu Ile Thr Lys Glu Leu Pro Lys Thr Leu Gln Asn Thr Lys
66 35 40 45
67 Asp Gln Pro Thr Ile Asp Lys Ile Phe Gln Asp Leu Asp Ala Asp Lys
68 50 55 60
69 Asp Gly Ala Val Ser Phe Glu Glu Phe Val Val Leu Val Ser Arg Val
70 65 70 75 80
71 Leu Lys Thr Ala His Ile Asp Ile His Lys
72 85 90

73 <210> SEQ ID NO 5

74 <211> LENGTH: 18

75 <212> TYPE: PRT

76 <213> ORGANISM: ARTIFICIAL SEQUENCE

77 <400> SEQUENCE: 5

78 Asp Gly Ala Val Ser Phe Glu Glu Phe Val Val Leu Val Ser Arg Val
79 1 5 10 15

80 Leu Lys

81 <210> SEQ ID NO 6

82 <211> LENGTH: 5

83 <212> TYPE: PRT

84 <213> ORGANISM: ARTIFICIAL SEQUENCE

85 <400> SEQUENCE: 6

86 Ala Gln Asn Ile Thr

87 1 5

PAGE: 3

VERIFICATION SUMMARY
PATENT APPLICATION US/09/167,705A

DATE: 11/26/1999
TIME: 16:17:47

Input Set: I167705A.RAW

Line ? Error/Warning

Original Text

35 W "N" or "Xaa" used: Feature required

Lys Gln Leu Gly Thr Lys Glu Leu Pro Lys T